1636

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             RAW SEQUENCE LISTING              DATE: 03/05/2001
             PATENT APPLICATION:  US/09/424,951   TIME: 15:43:55

             Input Set : A:\87714113.app
             Output Set: N:\CRF3\03052001\I424951.raw
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ENTERED
see p.5

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 3 <110> APPLICANT: SRIKANTHA, THYAGARAJAN
 4         SOLL, DAVID R.
 6 <120> TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,
 7         CANIK1, AND USE THEREOF
 9 <130> FILE REFERENCE: 087714/0113
11 <140> CURRENT APPLICATION NUMBER: 09/424,951
12 <141> CURRENT FILING DATE: 2000-01-20
14 <150> PRIOR APPLICATION NUMBER: PCT/US98/11658
15 <151> PRIOR FILING DATE: 1998-06-05
17 <150> PRIOR APPLICATION NUMBER: 60/048,914
18 <151> PRIOR FILING DATE: 1997-06-06
20 <160> NUMBER OF SEQ ID NOS: 7
22 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <211> LENGTH: 1254
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27 <213> ORGANISM: Candida albicans
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36   1               5                  10                  15
38 ctt gat aca gag ttg acr cag tac caa cga gag atg ttg tcg att gtg   96
39 Leu Asp Thr Glu Leu Thr Gln Tyr Gln Arg Glu Met Leu Ser Ile Val
40               20                  25                  30
42 cat aac ttg gca aat tcc ttg ttg acc att ata gac gat ata ttg gat  144
43 His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp
44           35                  40                  45
46 att tct aag att gag gcg aat aga atg acg gtg gaa cag att gat ttt  192
47 Ile Ser Lys Ile Glu Ala Asn Arg Met Thr Val Glu Gln Ile Asp Phe
48       50                  55                  60
50 tca tta aga ggg aca gtg ttt ggt gca ttg aaa acg tta gcc gtc aaa  240
51 Ser Leu Arg Gly Thr Val Phe Gly Ala Leu Lys Thr Leu Ala Val Lys
52   65                  70                  75                  80
54 gct att gaa aaa aac cta gac ttg acc tat caa tgt gat tca tcg ttt  288
55 Ala Ile Glu Lys Asn Leu Asp Leu Thr Tyr Gln Cys Asp Ser Ser Phe
56                   85                  90                  95
58 cca gat aat ctt att gga gat agt ttt aga tta cga caa gtt att ctt  336
59 Pro Asp Asn Leu Ile Gly Asp Ser Phe Arg Leu Arg Gln Val Ile Leu
60               100                 105                 110
62 aac ttg gct ggt aat gct att aag ttt act aaa gag ggg aaa gtt agt  384
63 Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Lys Glu Gly Lys Val Ser
64           115                 120                 125
66 gtt agt gtg aaa aag tct gat aaa atg gtg tta gat agt aag ttg ttg  432
67 Val Ser Val Lys Lys Ser Asp Lys Met Val Leu Asp Ser Lys Leu Leu
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68      130                   135                   140
70 tta gag gtt tgt gtt agc gac acg gga ata ggt ata gag aaa gac aaa   480
71 Leu Glu Val Cys Val Ser Asp Thr Gly Ile Gly Ile Glu Lys Asp Lys
72 145                   150                   155                   160
74 ttg gga ttg att ttc gat acc ttc tgt caa gct gat ggt tct act aca   528
75 Leu Gly Leu Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr
76                       165                   170                   175
78 aga aag ttt ggt ggt aca ggt tta ggg ttg tca att tcc aaa cag ttg   576
79 Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Gln Leu
80                       180                   185                   190
82 ata cat tta atg ggt gga gag ata tgg gtt act tcg gag tat gga tcc   624
83 Ile His Leu Met Gly Gly Glu Ile Trp Val Thr Ser Glu Tyr Gly Ser
84         195                   200                   205
86 ggr tca aac ttt tat ttt acg gtg tgc gtg tcg cca tct aat att aga   672
87 Gly Ser Asn Phe Tyr Phe Thr Val Cys Val Ser Pro Ser Asn Ile Arg
88         210                   215                   220
90 tat act cga caa acc gaa caa ttg tta cca ttt agt tcc cat tat gtg   720
91 Tyr Thr Arg Gln Thr Glu Gln Leu Leu Pro Phe Ser Ser His Tyr Val
92 225                   230                   235                   240
94 tta ttt gta tcg act gag cat act caa gaa gaa ctt gat gtg ttg aga   768
95 Leu Phe Val Ser Thr Glu His Thr Gln Glu Glu Leu Asp Val Leu Arg
96                       245                   250                   255
98 gat gga att ata gaa ctt gga ttg ata cct ata ata gtg aga aat att   816
99 Asp Gly Ile Ile Glu Leu Gly Leu Ile Pro Ile Ile Val Arg Asn Ile
100                      260                   265                   270
102 gaa gat gca aca ttg act gag ccg gtg aaa tat gat ata att atg att   864
103 Glu Asp Ala Thr Leu Thr Glu Pro Val Lys Tyr Asp Ile Ile Met Ile
104         275                   280                   285
106 gat tcg ata gag att gcc aaa aag ttg agg ttg tta tcg gag gtt aaa   912
107 Asp Ser Ile Glu Ile Ala Lys Lys Leu Arg Leu Leu Ser Glu Val Lys
108         290                   295                   300
110 tat att ccg ttg gtt ttg gtc cat cat tct att cca cag ttg aat atg   960
111 Tyr Ile Pro Leu Val Leu Val His His Ser Ile Pro Gln Leu Asn Met
112 305                   310                   315                   320
114 aga gta tgt att gat ttg ggg ata tct tcc tat gca aat acg cca tgt   1008
115 Arg Val Cys Ile Asp Leu Gly Ile Ser Ser Tyr Ala Asn Thr Pro Cys
116                      325                   330                   335
118 tcg atc acg gac ttg gcc agt gcg att ata cca gcg ttg gag tcg aga   1056
119 Ser Ile Thr Asp Leu Ala Ser Ala Ile Ile Pro Ala Leu Glu Ser Arg
120         340                   345                   350
122 tct ata tca cag aac tca gac gag tcg gtg agg tac aaa ata tta cta   1104
123 Ser Ile Ser Gln Asn Ser Asp Glu Ser Val Arg Tyr Lys Ile Leu Leu
124         355                   360                   365
126 gca gag gac aac ctc gtc aat cag aaa ctt gca gtt agg ata tta gaa   1152
127 Ala Glu Asp Asn Leu Val Asn Gln Lys Leu Ala Val Arg Ile Leu Glu
128         370                   375                   380
130 aag caa ggg cat ctg gtg gaa gta gtt gag aac gga ctc gag gcg tac   1200
131 Lys Gln Gly His Leu Val Glu Val Val Glu Asn Gly Leu Glu Ala Tyr
132 385                   390                   395                   400
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RAW SEQUENCE LISTING   DATE: 03/05/2001
PATENT APPLICATION: US/09/424,951   TIME: 15:43:55

     Input Set : A:\87714113.app
     Output Set: N:\CRF3\03052001\I424951.raw

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134 gaa gcg att aag agg aat aaa tat gat gtg gtg ttg atg gat gtg caa     1248
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138 atg cct                                                             1254
139 Met Pro
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 418
144 <212> TYPE: PRT
145 <213> ORGANISM: Candida albicans
147 <400> SEQUENCE: 2
148 Glu Ile Arg Thr Pro Leu Asn Gly Ile Ile Gly Met Thr Gln Leu Ser
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151 Leu Asp Thr Glu Leu Thr Gln Tyr Gln Arg Glu Met Leu Ser Ile Val
152             20                  25                  30
154 His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp
155         35                  40                  45
157 Ile Ser Lys Ile Glu Ala Asn Arg Met Thr Val Glu Gln Ile Asp Phe
158      50                  55                  60
160 Ser Leu Arg Gly Thr Val Phe Gly Ala Leu Lys Thr Leu Ala Val Lys
161  65                  70                  75                  80
163 Ala Ile Glu Lys Asn Leu Asp Leu Thr Tyr Gln Cys Asp Ser Ser Phe
164              85                  90                  95
166 Pro Asp Asn Leu Ile Gly Asp Ser Phe Arg Leu Arg Gln Val Ile Leu
167             100                 105                 110
169 Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Lys Glu Gly Lys Val Ser
170         115                 120                 125
172 Val Ser Val Lys Lys Ser Asp Lys Met Val Leu Asp Ser Lys Leu Leu
173         130                 135                 140
175 Leu Glu Val Cys Val Ser Asp Thr Gly Ile Gly Ile Glu Lys Asp Lys
176 145                 150                 155                 160
178 Leu Gly Leu Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr
179             165                 170                 175
181 Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Gln Leu
182             180                 185                 190
184 Ile His Leu Met Gly Gly Glu Ile Trp Val Thr Ser Glu Tyr Gly Ser
185         195                 200                 205
187 Gly Ser Asn Phe Tyr Phe Thr Val Cys Val Ser Pro Ser Asn Ile Arg
188         210                 215                 220
190 Tyr Thr Arg Gln Thr Glu Gln Leu Leu Pro Phe Ser Ser His Tyr Val
191 225                 230                 235                 240
193 Leu Phe Val Ser Thr Glu His Thr Gln Glu Glu Leu Asp Val Leu Arg
194             245                 250                 255
196 Asp Gly Ile Ile Glu Leu Gly Leu Ile Pro Ile Ile Val Arg Asn Ile
197             260                 265                 270
199 Glu Asp Ala Thr Leu Thr Glu Pro Val Lys Tyr Asp Ile Ile Met Ile
200         275                 280                 285
202 Asp Ser Ile Glu Ile Ala Lys Lys Leu Arg Leu Leu Ser Glu Val Lys
203         290                 295                 300
205 Tyr Ile Pro Leu Val Leu Val His His Ser Ile Pro Gln Leu Asn Met
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RAW SEQUENCE LISTING   DATE: 03/05/2001
PATENT APPLICATION: US/09/424,951   TIME: 15:43:55

Input Set : A:\87714113.app
Output Set: N:\CRF3\03052001\I424951.raw

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206 305                 310              315              320
208 Arg Val Cys Ile Asp Leu Gly Ile Ser Ser Tyr Ala Asn Thr Pro Cys
209             325              330                  335
211 Ser Ile Thr Asp Leu Ala Ser Ala Ile Ile Pro Ala Leu Glu Ser Arg
212             340              345                  350
214 Ser Ile Ser Gln Asn Ser Asp Glu Ser Val Arg Tyr Lys Ile Leu Leu
215         355              360                  365
217 Ala Glu Asp Asn Leu Val Asn Gln Lys Leu Ala Val Arg Ile Leu Glu
218     370              375                  380
220 Lys Gln Gly His Leu Val Glu Val Val Glu Asn Gly Leu Glu Ala Tyr
221 385              390                  395                  400
223 Glu Ala Ile Lys Arg Asn Lys Tyr Asp Val Val Leu Met Asp Val Gln
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231 <211> LENGTH: 3246
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233 <213> ORGANISM: Candida albicans
235 <220> FEATURE:
236 <221> NAME/KEY: CDS
237 <222> LOCATION: (1)..(3243)
239 <400> SEQUENCE: 3
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242  1                5                  10                  15
244 ttt gaa ata ctc aac gac cct gag ctt tat agt cag cac tgt cat agc    96
245 Phe Glu Ile Leu Asn Asp Pro Glu Leu Tyr Ser Gln His Cys His Ser
246                 20                  25                  30
248 ctt agg gaa aca ctt ctt gat cat ttc aac cat caa gct aca ctt atc   144
249 Leu Arg Glu Thr Leu Leu Asp His Phe Asn His Gln Ala Thr Leu Ile
250             35                  40                  45
252 gac act tat gaa cat gaa cta gaa aaa tcc aaa aat gcc aac aaa gcg   192
253 Asp Thr Tyr Glu His Glu Leu Glu Lys Ser Lys Asn Ala Asn Lys Ala
254     50                  55                  60
256 tcc caa caa gca ctt agt gaa ata ggt aca gtt gtt ata tct gtt gcc   240
257 Ser Gln Gln Ala Leu Ser Glu Ile Gly Thr Val Val Ile Ser Val Ala
258  65                  70                  75                  80
260 atg gga gac ttg tcg aaa aaa gtt gag att cac aca gta gaa aat gac   288
261 Met Gly Asp Leu Ser Lys Lys Val Glu Ile His Thr Val Glu Asn Asp
262                 85                  90                  95
264 cct gag att tta aaa gtc aaa atc acc atc aac acc atg atg gat caa   336
265 Pro Glu Ile Leu Lys Val Lys Ile Thr Ile Asn Thr Met Met Asp Gln
266             100                 105                 110
268 tta cag aca ttt gct aat gag gtt aca aaa gtc gcc acc gaa gtc gca   384
269 Leu Gln Thr Phe Ala Asn Glu Val Thr Lys Val Ala Thr Glu Val Ala
270         115                 120                 125
272 aat ggt gaa cta ggt gga caa gcg aaa aat gat gga tct gtt ggt att   432
273 Asn Gly Glu Leu Gly Gly Gln Ala Lys Asn Asp Gly Ser Val Gly Ile
274     130                 135                 140
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276 tgg aga tca ctt aca gac aat gtt aat att atg gct ctt aat tta act   480
277 Trp Arg Ser Leu Thr Asp Asn Val Asn Ile Met Ala Leu Asn Leu Thr
278 145                 150                 155                 160
280 aac caa gtg cga gaa att gct gat gtc aca cgt gct gtt gcc aag ggg   528
281 Asn Gln Val Arg Glu Ile Ala Asp Val Thr Arg Ala Val Ala Lys Gly
282                 165                 170                 175
284 gac ttg tca cgt aaa att aat gta cac gcc cag ggt gaa atc ctt caa   576
285 Asp Leu Ser Arg Lys Ile Asn Val His Ala Gln Gly Glu Ile Leu Gln
286                 180                 185                 190
288 ctt caa cgt aca ata aac acc atg gtg gat cag tta cga acg ttt gca   624
289 Leu Gln Arg Thr Ile Asn Thr Met Val Asp Gln Leu Arg Thr Phe Ala
290                 195                 200                 205
292 ttc gaa gta tct aaa gtt gct aga gat gtt ggt gtg ctt ggt ata tta   672
293 Phe Glu Val Ser Lys Val Ala Arg Asp Val Gly Val Leu Gly Ile Leu
294     210                 215                 220
296 gga gga caa gcg ttg att gaa aat gtt gaa ggt att tgg gaa gag ttg   720
297 Gly Gly Gln Ala Leu Ile Glu Asn Val Glu Gly Ile Trp Glu Glu Leu
298 225                 230                 235                 240
300 act gat aat gtc aat gcc atg gct ctt aat ttg act aca caa gtg aga   768
301 Thr Asp Asn Val Asn Ala Met Ala Leu Asn Leu Thr Thr Gln Val Arg
302                 245                 250                 255
304 aat att gcc aat gtc acc act gcc gtt gcc aag ggg gat ttg tcg aaa   816
305 Asn Ile Ala Asn Val Thr Thr Ala Val Ala Lys Gly Asp Leu Ser Lys
306                 260                 265                 270
308 aaa gtc act gct gat tgt aag gga gaa aty ctt gat ttg aaa ctt act   864
309 Lys Val Thr Ala Asp Cys Lys Gly Glu Ile Leu Asp Leu Lys Leu Thr
310             275                 280                 285
312 att aat caa atg gtg gac cga tta cag aat ttt gct ctt gcg gtg acg   912
313 Ile Asn Gln Met Val Asp Arg Leu Gln Asn Phe Ala Leu Ala Val Thr
314     290                 295                 300
316 aca ttg tcg aga gag gtt ggt act ttg ggt att ttg ggt gga caa gct   960
317 Thr Leu Ser Arg Glu Val Gly Thr Leu Gly Ile Leu Gly Gly Gln Ala
318 305                 310                 315                 320
320 aac gta cag gat gtt gaa ggt gct tgg aaa cag gtt aca gaa aat gtc   1008
321 Asn Val Gln Asp Val Glu Gly Ala Trp Lys Gln Val Thr Glu Asn Val
322                 325                 330                 335
324 aac cta atg gct act aat tta act aac caa gtg aga tct att gct aca   1056
325 Asn Leu Met Ala Thr Asn Leu Thr Asn Gln Val Arg Ser Ile Ala Thr
326                 340                 345                 350
328 gtt act act gca gtt gcg cat ggt gat ttg tcg caa aag att gat ggt   1104
329 Val Thr Thr Ala Val Ala His Gly Asp Leu Ser Gln Lys Ile Asp Gly
330             355                 360                 365
332 cat ccc aaa gga gag att tta caa ttg aaa aat aca atc aac aag atg   1152
333 His Pro Lys Gly Glu Ile Leu Gln Leu Lys Asn Thr Ile Asn Lys Met
334     370                 375                 380
336 gtg gac tct ttg cag ttg ttt gca tca gaa gtg tcg aaa gtg gca caa   1200
337 Val Asp Ser Leu Gln Leu Phe Ala Ser Glu Val Ser Lys Val Ala Gln
338 385                 390                 395                 400
340 gat gtt ggt att aat gga aaa tta ggt att caa gca caa gtt agt gat   1248
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Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 03/05/2001
PATENT APPLICATION: US/09/424,951   TIME: 15:43:57

Input Set : A:\87714113.app
Output Set: N:\CRF3\03052001\I424951.raw

L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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